

IN THE SPECIFICATION:

On page 1, please replace the paragraph spanning lines 9-12 with the following amended paragraph:

This application is a continuation of U.S. Patent Application Serial No. 09/802,213, filed March 8, 2001, now U.S. Patent No. 6,630,313 which claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Provisional Application Serial No. 60/188,930, filed March 8, 2000, and entitled "Product and Method for Regulation of Inflammation." The entire disclosure of each of U.S. Provisional Application Serial No. 60/188,930 and U.S. Patent Application Serial No. 09/802,213 is incorporated herein by reference.

Please replace the paragraph spanning page 24, line 24 to page 25, line 12, the the following amended paragraph:

As used herein, unless otherwise specified, reference to a percent (%) identity refers to an evaluation of homology which is performed using a BLAST homology search. BLAST homology searches can be performed using the BLAST database and software, which offers search programs including: (1) a BLAST 2.0 Basic BLAST homology search available through the National Center for Biotechnology Information (division of the National Library of Medicine and the National Institutes of Health), (<http://www.ncbi.nlm.nih.gov/BLAST>) using blastp for amino acid searches and blastn for nucleic acid searches with standard default parameters, wherein the query sequence is filtered for low complexity regions by default (described in Altschul, S.F., Madden, T.L., Schääffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402, incorporated herein by reference in its entirety); (2) a BLAST 2 alignment (using the parameters described below) (<http://www.ncbi.nlm.nih.gov/BLAST>); (3) and/or PSI-BLAST with the standard default parameters (Position-Specific Iterated BLAST; (<http://www.ncbi.nlm.nih.gov/BLAST>)). It is noted that due to some differences

in the standard parameters between BLAST 2.0 Basic BLAST and BLAST 2, two specific sequences might be recognized as having significant homology using the BLAST 2 program, whereas a search performed in BLAST 2.0 Basic BLAST using one of the sequences as the query sequence may not identify the second sequence in the top matches.